SEQUENCE LISTING

<110> Clendennen, Stephanie K.
      Schuster, Debra K.

<120> CTR1 HOMOLOGUE FROM MELON

<130> 4257-0029.30

<140> Not Yet Assigned
<141> Filed Herewith

<150> US 60/218,307
<151> 2000-07-14

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 3286
<212> DNA
<213> Cucumis melo

<220>
<221> misc_feature
<222> (81)...(81)
<223> n = A,T,C or G

<220>
<221> misc_feature
<222> (593)...(594)
<223> n = A,T,C or G

<400> 1

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ccggacgagg aggttggaac gggagcttcc acttcctttt acgactccgt agcagctggg     240
ggaaacgtta tcaaagggag aaccgatagg gttttttgatt gggatgggag tggtgatcac     300
aggttaaaca cgcaggcgta tcggataggg aacctgtatt catggattgg tttacagaga     360
cattccagtg gaagcagcta cgatgatagc tctctctcta gtgattacta cgcaccgacg     420
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gccgatgatc ccaactttat ggatccgatt ccagacgagg cagctttaag atcgttatcg     660
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ttcaggtcac tggccaaaca gtatttcttg gatagccaat cacttaatct tgtatttgat    1440
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1

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<210> 2
<211> 850
<212> PRT
<213> Cucumis melo

<220>
<221> VARIANT
<222> (154)...(154)
<223> Xaa = Any Amino Acid

<400> 2
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Val Ala Ala Gly Gly Asn Val Ile Lys Gly Arg Thr Asp Arg Val Phe
        35                  40                  45
Asp Trp Asp Gly Ser Gly Asp His Arg Leu Asn Thr Gln Ala Tyr Arg
    50                  55                  60
Ile Gly Asn Leu Tyr Ser Trp Ile Gly Leu Gln Arg His Ser Ser Gly
65                  70                  75                  80
Ser Ser Tyr Asp Asp Ser Ser Leu Ser Ser Asp Tyr Tyr Ala Pro Thr
                85                  90                  95
Leu Ser Asn Pro Ala Ala Asn Glu Ile Asn Ala Leu Glu Tyr Ile Leu
            100                 105                 110
Asp Asp Asp Phe Arg Val Met Lys Ala Val Gly Ser Gly Gly Ser Ser
            115                 120                 125
Gly Lys Ser Trp Ala Gln Gln Thr Glu Glu Ser Phe Gln Leu Gln Gln
    130                 135                 140
Pro Leu Val Leu Arg Leu Ser Ser Asp Xaa Thr Cys Ala Asp Asp Pro
145                 150                 155                 160
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```
Asn Phe Met Asp Pro Ile Pro Asp Glu Ala Ala Leu Arg Ser Leu Ser
            165                 170                 175
Ile Ser Ala Glu Ala Ile Ser His Arg Phe Trp Val Asn Gly Cys Met
            180                 185                 190
Ser Tyr Leu Glu Lys Val Pro Asp Gly Phe Tyr Leu Ile His Gly Met
            195                 200                 205
Asp Pro Tyr Val Trp Ser Leu Cys Thr Asn Leu Gln Glu Asp Gly Arg
    210                 215                 220
Ile Pro Ser Phe Glu Ser Leu Lys Thr Val Asp Ser Ser Ile Gly Ser
225                 230                 235                 240
Ser Ile Glu Val Val Leu Ile Asp Arg His Ser Asp Ala Ser Leu Lys
            245                 250                 255
Glu Leu Gln Asn Arg Val His Asn Ile Ser Ser Ser Cys Val Thr Thr
            260                 265                 270
Lys Glu Val Ala Asp His Ile Ala Lys Leu Val Cys Asn His Leu Gly
            275                 280                 285
Gly Ser Val Ser Glu Gly Glu Asp Asp Leu Val Ser Ala Trp Lys Glu
    290                 295                 300
Cys Ser Asp Asp Leu Lys Glu Cys Leu Gly Ser Ala Val Ile Pro Leu
305                 310                 315                 320
Cys Ser Leu Ser Val Gly Leu Cys Arg His Arg Ala Leu Leu Phe Lys
            325                 330                 335
Val Leu Ala Asp Ser Ile Asp Leu Pro Cys Arg Ile Ala Lys Gly Cys
            340                 345                 350
Lys Tyr Cys Thr Arg Asp Asp Ala Ser Ser Cys Leu Val Arg Phe Gly
    355                 360                 365
Leu Asp Arg Glu Tyr Leu Ile Asp Leu Ile Gly Arg Pro Gly Cys Leu
    370                 375                 380
Cys Gln Pro Asp Ser Leu Leu Asn Gly Pro Ser Ser Ile Ser Ile Ser
385                 390                 395                 400
Ser Pro Leu Arg Phe Pro Arg Leu Lys Pro Ile Glu Ser Thr Ile Asp
            405                 410                 415
Phe Arg Ser Leu Ala Lys Gln Tyr Phe Leu Asp Ser Gln Ser Leu Asn
            420                 425                 430
Leu Val Phe Asp Glu Ala Ser Ser Gly Asn Val Val Ser Gly Lys Asp
            435                 440                 445
Ala Ala Phe Ser Val Tyr Gln Arg Pro Leu Asn Arg Lys Asp Val Asp
    450                 455                 460
Gly Lys Thr Ile Val Val Thr Gly Asp Lys Asp Arg Asn Ser Gln Leu
465                 470                 475                 480
Leu Asn Lys Lys Ala Ala Gln Leu Asn Thr Gln Asp Gly Lys Ser Glu
            485                 490                 495
Gln Phe Arg Ser Cys Val Ala Ser Pro Tyr Ser Val Gln Ser Thr Pro
            500                 505                 510
Phe Val Glu Asn Val Val Pro Leu Ser His Ile Ser His Ile Gly Ser
            515                 520                 525
Glu Asp Ser Glu His Leu Leu Ala Leu Ser His Pro Arg Met Asp His
            530                 535                 540
Val Asn Asn Leu Pro Phe Val His Gly Ser Gln Leu Ile Arg Lys Pro
545                 550                 555                 560
Asn Glu Leu Ser Leu Gly Leu Glu Asp Leu Val Ile Pro Trp Thr Asp
            565                 570                 575
Leu Asp Leu Arg Glu Lys Ile Gly Ala Gly Ser Phe Gly Thr Val Tyr
            580                 585                 590
Arg Gly Glu Trp His Gly Ser Asp Val Ala Val Lys Ile Leu Thr Glu
            595                 600                 605
Gln Asp Phe His Pro Glu Arg Val Asn Glu Phe Leu Arg Glu Val Ala
    610                 615                 620
Ile Met Lys Ser Leu Arg His Pro Asn Ile Val Leu Phe Met Gly Ala
625                 630                 635                 640
Val Thr Lys Pro Pro Asn Leu Ser Ile Val Thr Glu Tyr Leu Ser Arg
            645                 650                 655
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                                    3

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Gly Ser Leu Tyr Arg Leu Leu His Lys Ser Gly Val Lys Asp Ile Asp
            660                 665             670
Glu Thr Arg Arg Ile Asn Met Ala Phe Asp Val Ala Lys Gly Met Asn
        675             680             685
Tyr Leu His Arg Arg Asp Pro Pro Ile Val His Arg Asp Leu Lys Ser
    690             695             700
Pro Asn Leu Leu Val Asp Lys Lys Tyr Thr Val Lys Val Cys Asp Phe
705             710             715             720
Gly Leu Ser Arg Leu Lys Ala Arg Thr Phe Leu Ser Ser Lys Ser Ala
            725             730             735
Ala Gly Thr Pro Glu Trp Met Ala Pro Glu Val Leu Arg Asp Glu Pro
            740             745             750
Ser Asn Glu Lys Ser Asp Val Tyr Ser Phe Gly Val Ile Leu Trp Glu
        755             760             765
Leu Ala Thr Leu Gln Gln Pro Trp Cys Asn Leu Asn Pro Ala Gln Val
    770             775             780
Val Ala Ala Val Gly Phe Lys Gly Lys Arg Leu Asp Ile Pro Arg Asp
785             790             795             800
Val Asn Pro Lys Leu Ala Ser Leu Ile Val Ala Cys Trp Ala Asp Glu
            805             810             815
Pro Trp Lys Arg Pro Ser Phe Ser Ser Ile Met Glu Thr Leu Lys Pro
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Met Thr Lys Gln Ala Pro Pro Gln Gln Ser Arg Thr Asp Thr Leu Ser
            835             840             845
Val Met
    850
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<210> 3
<211> 28
<212> DNA
<213> sArtificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 3
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<210> 4
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 4
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<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 5
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<210> 6
<211> 24
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<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 6
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<210> 7
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 7
catgtgttgc ttctccatat agtg   24

<210> 8
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic oligonucleotide

<400> 8
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